

F I G. 1 A

-300

-320

-340

-280

CACTCGTCTGCCCTGGACTCCCGTCTCCTGTCCTCCGGCTTCCCAGAGCTCCCTCC  
+---+---+---+---+---+---+---+---+---+---+---+  
GTGACCGACGGGACCTGAGGGCAGGGAGGACAGGGCCAAAGGGCTCTGACGGGAGG  
-260 -240 -220

TTATGGCAGCAGCTTCCCGCTCTCCGGCTCAAGCTCAGCGACCGACCCTCTGCTCCG  
+---+---+---+---+---+---+---+---+---+---+---+  
AATAACGTCGTAAGGGCGCAGAGCCGCTCAAGAGTCGGCTGCTGGAGAGGGAGGGC  
-200 -180 -160

GGGCTGAGCCCCAGTCCCTGGATCTTGCTGAAACTCTCGAGATCATGCCGGGTTCGGCTG  
+---+---+---+---+---+---+---+---+---+---+---+  
CCCGACTCGGGTCAGGGACCTAACCGACTTGTAGAGCTCTAGTACGGCCCAAACCGAC  
-140 -120 -100

CTGGCTTCCCGGGGGCCACTGCCACCCGGCCCTCTGCTGCCGGGGCTCCGGGGGA  
+---+---+---+---+---+---+---+---+---+---+---+  
GACGAAGGGGGCCACGGGTGACGGTGGGGAGACGACGGGGAGGGCAGGGCCCT  
-80 -60 -40

TGCTCAGTAGCCCCGCTGCCGGCCCCCGGATCCTCTTCCGAAAGCCGTTGCCCTG  
+---+---+---+---+---+---+---+---+---+---+---+  
ACGAGTCATGGGGACGGGGGGGGCTAGGACACAAGGAGGCCTTCGGCAAACGACG  
-20 0 20

MATCH WITH FIG. 1B

MATCH WITH FIG. 1A

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CTGTAATTGATGGGAATGTAAAGAATTGGAGACACTGTGACTTGCCTCTGTCAGTT  
MATCH WITH FIG. 1C

MATCH WITH FIG. 1B FIG. 1C

GACATTAAACTACCCCTTACAATTCTAACCTTAACCTCTGTGACACTGAACGCCAGACAGTCAA  
 C K F D G E C L R I G D T V T C V C Q F  
 280 300 320  
 CAAGTGCACAACTGACTATGTGCCCTGTTGGCTCCAAATGGGGAGGCTTACCAAGAATGAG  
 GTTCACGTTGTTACTGATAACGGACACACCCGAGGTACCCCTCTCGATGGTCTTACT  
 K C N N D Y V P V C G S N G E S Y Q N E  
 340 360 380  
 GTGTTACCTGCCACAGGCTGCATGCCAAACAGCAGAGTGAAGATACTTGTGGTGTGAGAGG  
 CACAAATGGACGGCTGTCGGCACGGTACGGTTACTGTTACTCTACACTCTATGAAACACCACAGTCTTCC  
 C Y L R Q A A C K Q S E I L V V S E G  
 400 420 440  
 ATCATGGCCACAGATGCCAGGATCAGGATCTGGAGATGGAGATCTGGTGTGAGTCCATGAAAGGCTCTGGAGA  
 TAGTACACGGCTGCTACGCTCCTAGACCTCTACCTCAGGTACTTCCGAGAACCTCT  
 S C A T D A G S G D G V H E G S G E  
 460 480 500  
 AACTAGTCAAAAGGAGACATCCACCTGTGATATTGCCAGTTGGTGCAGAAATGTGACGAA  
 TTGATCAGTTCTCTGTAGGTGGACACTATAACGGTCAAACCGTCTTACACTGCT  
 MATCH WITH FIG. 1D

MATCH WITH FIG. 1C  
T S Q K E T S T C D I C Q F G A E 560  
520

AGATGCCGAGGATGTCTGGTGTGTTAATTTGACTGTCTCAAACCAACTTCATCC  
 TCTACGGCTCCTACAGACACCACACATTTAACTGACAAGAGTTGGTGAAGTTAGG  
 D A E D V W C V C N I D C S Q T N F N P  
 580 600 620  
 CCTCTGCCCTCTGATGGAAATTCTTATGATAATGCCAAATCAAAAGAACCATCGTG  
 GGAGACGGAAAGACTACCCCTTACGAAATACTTACGTTACCGTTAGTTCTTCGTTAGCAC  
 L C A S D G K S Y D N A C Q I K E A S C  
 640 660 680  
 TCAAGAACAGGAGAAAATTGAAAGTCATGTCCTTGGCTCGATGTCAGATAACACACTAC  
 AGTCTTGTCTCTTTAACTTCAGTACAGAAACCCAGCTACAGTTCTATTTGTTGATG  
 Q K Q E K I E V M S L G R C Q D N T T T  
 700 720 740  
 AACTACTAAGTCTGAAGATGGCCATTATCCAAGAACAGATTATGCAAGAGAATGCTAACAA  
 TIGATGATTCAAGACTTCTACCCGTTAATACGTTCTTAATACGGTCTTACGATTGTT  
 T T K S E D G H Y A R T D Y A E N A N K  
 760 780 800

MATCH WITH FIG. 1E

MATCH WITH FIG. 1D

FIG. 1E

ATAGAAGAAAGTGCCAGAACACCATACCTTGTCCGGAACATTACAATGGCTTCCTG  
TAATCTTCTTTACGGGTCTTGTGTATGGAACAGGCCTTGTAATGTTACCGAAC  
L E S A R E H H I P C P E H Y N G F C  
820 860

CATGCCATGGAAAGTGTGAGCATTCAATTATGCAGGAGCCATCTTGCAGGTGATGCC  
GTACGTACCCCTTCACACTCGTAAGATAAGATTTACGTCTCGCTAGAACGTCCACACTACGG  
M H G K C E H S I N M Q E P S C R C D A  
880 920

TGGTTATACTGGACAAACACTGTGAAAAAGGAACTACAGTGTCTATACGTTGTTCCCCGG  
ACCAAATGACCTGTTGTGACACTTTTCTGATGTCACAAGATATGCAACAAAGGGCC  
G Y T G Q H C E K K D Y S V L Y V V P G  
940 980

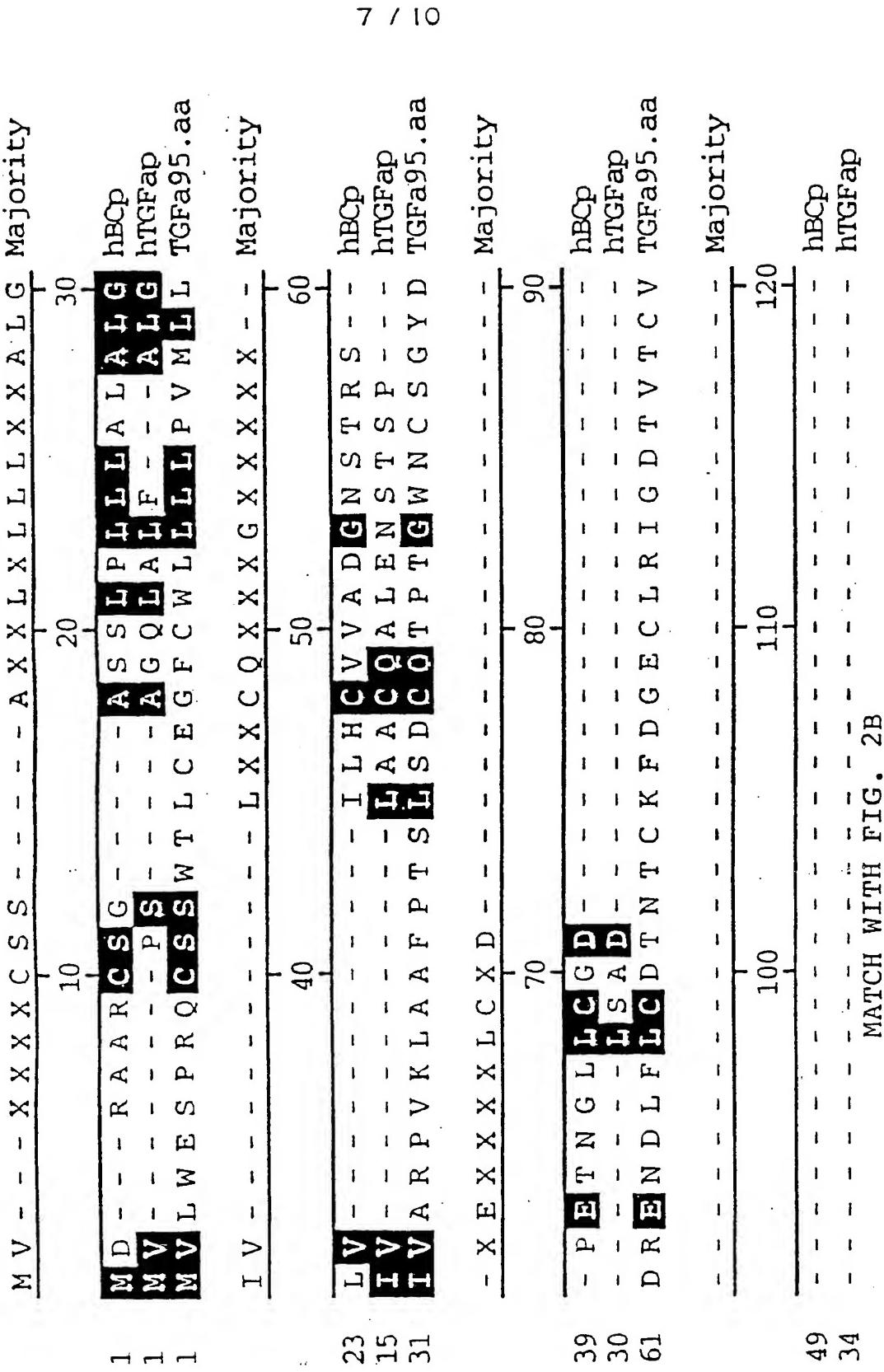
TCCTGTACGATTCACTATGCTTTAATCGCAGCTGTGATGGAACATTCAAGATTGCTGT  
AGGACATGCTAAAGTCATACAGAAATTAGCGGTGACACTAACCTTGTTAAGTCTAACGACA  
P V R F Q Y V L I A V I G T I Q I A V  
1000 1040

CATCTGTGGTGGTCTGATCACAAAGGAATGCCAGAACAGAAATTCAACAG  
GTAGACACACCAGGAGACGTAGTGTCTTACGGGGTCTTCGTTGCTTAAGTGT  
MATCH WITH FIG. 1F

## MATCH WITH FIG. 1E

I	C	V	V	L	C	I	T	R	K	C	P	R	S	N	R	I	H	R	
1060	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	1100
ACAGAAGCAAATAACAGGGCACTACAGTTTCGGACAATAACAAAGAGCCGTCACAGGGTT																			
TGTCTCGTTTATGTCCCCGTATGTCAGGCCTGTTATGTTCTCGAGGTGCTCCAA																			
Q	K	N	T	G	H	Y	S	S	D	N	T	T	R	A	S	T	R	L	
1120	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	1160	
AATCTAACGGGAGCATGTTTCACAGTGGCAGACTACCGAGAGCTGGACTACACAATAC																			
TTAGATTCCCTCGTACAAAGTGTACACCGACCTGATEGCCCTCGAACCTGATGTGTTATG																			
I	*	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	
1180	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	1220	
AGTATTATAGACAAAGAACATAAGACAAAGAGATCTACACATGTTGCCATTGCTTGGA																			
TCATAATATCTGTTTCTTATTCCTGTTCTAGATGTTGATACAACGGAACGTTAACACCAT																			
1240	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	1280	
ATCTACACCAATGAAAACATGTACTACAGCTATATTGATTATGTTGATATTTGAA																			
TAGATGTCGTTACTTTGTACATGATGTCGATATAACATAACATATAACTT																			
1300	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	1340	
ATAGTATACTGTCTGATGTTTCTGTAATGTAATAACTATATATCACACAA																			
TATCATATGTAACAGAACTACACAAAGACATTACATTATTGATAAAATATAGTGTGTT																			
1360	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	1400	
AAAAAA																			
TTTTTTTTTTTTTT																			

FIG. 2 A



MATCH WITH FIG. 2A

FIG. 2 B

MATCH WITH FIG. 2A  
91 C Q F K C N N D Y V P V C G S N G E S Y Q N E C Y L R Q A A T G F a 95. aa

	Majority		
	160	170	180
56	- - -	- - -	- - -
41	- - -	- - -	- - -
151	S G E T S Q K E T S T C D I C Q F G A E C D E D A E D V W C	T G F a 9 5 . a a	h B Q P

		Majority
56	- - - - -	hBCP
41	- - - - -	hTGFap
181	V C N I D C S Q T N F N P L C A S D G K S Y D N A C Q I K E T G F a 9 5 . a a	

MATCH WITH FIG. 2C

MATCH WITH FIG. 2B

FIG. 2 C

56	-	-	-	-	-	-	-	T T T Q S K R K G	hBCP
41	-	-	-	-	-	-	-	hTGFap	
211	A	S	C	Q	K	Q	E	V M S L G R C Q D N T T T T T K S E D G	TGFa95.aa
H F X R	-	-	-	-	-	-	-	-	Majority
65	H	F	S	R	-	-	-	-	250
43	H	F	N	D	-	-	-	-	
241	H	Y	A	R	T	D Y A E N A N K L E E S A R E H H I P C			
X F C X H G X C R F X V X E Q X P S C V C D X G Y X G A R C									
75	H	Y	C	I	K	G	R	C R F V V A E Q T P S C V C D E G Y I G A R C	hBCP
53	O	F	C	F	H	G	T	C R F L V Q E D K P A C V C H S G Y V G A R C	hTGFap
271	G	F	C	M	H	G	K	C E H S I N M Q E P S C R C D A G Y T G Q H C	TGFa95.aa
X X D L X X L X X X G X X X I X X L I A V X I V X I X									
105	E	R	D	L	F	Y	L	R G D R C Q I L V I L I A V M V F I I	hBCP
83	E	H	D	L	L	V	V	A S Q K K Q A I T A I V V V S I V A L A	hTGFap
301	E	K	D	Y	S	V	L	P V R F Q Y V I V I A V I Q G T I Q	TGFa95.aa
E X X D L X X L X X X G X X X I X X L I A V X I V X I X									
105	E	R	D	L	F	Y	L	R G D R C Q I L V I L I A V M V F I I	hBCP
83	E	H	D	L	L	V	V	A S Q K K Q A I T A I V V V S I V A L A	hTGFap
301	E	K	D	Y	S	V	L	P V R F Q Y V I V I A V I Q G T I Q	TGFa95.aa

MATCH WITH FIG. 2D

## MATCH WITH FIG. 2C

## F | G. 2D

	X X I X X C V X X X C C X - X R K X C X R X X X X X E	Majority
		360
		350
		340
134	L V <b>I</b> G V <b>C</b> T - - <b>C</b> C H P L R K R K R K - - - K E E	hBCP
113	V L <b>I</b> I T <b>C</b> V L I H <b>C</b> C Q - V R K H <b>C</b> E W C R A L I C R H E	htGFAp
331	I A V - I <b>C</b> V V V L <b>C</b> - - I T R K <b>C</b> P <b>R</b> S N R I H R Q K Q TGFa95.aa	TGFa95.aa
		370
		380
		390
157	E M E T <b>L</b> G K D <b>I</b> T P I N E D I E E T N <b>I</b> A	hBCP
142	K P S A <b>L</b> K G R <b>T</b> A C - - C H S E T V V	htGFAp
357	N T G H Y S S <b>D</b> N <b>T</b> T - - R A S T R L <b>I</b>	TGFa95.aa

Decoration 'Decoration #1': Shade with solid residues that match the Consensus exactly.